

JUL 08 2002

TECH CENTER 1600/2900



1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/325,278A

DATE: 06/10/2002
TIME: 16:22:34

Input Set : A:\402.app
Output Set: N:\CRF3\06102002\H325278A.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:
C--> 6 (i) APPLICANT: Bjorck, Lars
7 Sjobring, Ulf
9 (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
11 (iii) NUMBER OF SEQUENCES: 15
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Seed IP Law Group
15 (B) STREET: 701 Fifth Avenue Suite 6300
16 (C) CITY: Seattle
17 (D) STATE: Washington
18 (E) COUNTRY: USA
19 (F) ZIP: 98104-7092
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/08/325,278A
C--> 29 (B) FILING DATE: 26-Oct-1994
30 (C) CLASSIFICATION:
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Potter, Jane E. R.
34 (B) REGISTRATION NUMBER: 33,332
35 (C) REFERENCE/DOCKET NUMBER: 100084.402
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (206) 622-4900
39 (B) TELEFAX: (206) 682-6031
42 (2) INFORMATION FOR SEQ ID NO: 1:
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 305 amino acids
46 (B) TYPE: amino acid
47 (C) STRANDEDNESS: unknown
48 (D) TOPOLOGY: unknown
50 (ii) MOLECULE TYPE: protein
52 (iii) HYPOTHETICAL: NO
54 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
62 1 5 10 15
64 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser

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65 20 25 30
67 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
68 35 40 45
70 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asn Gly Glu Tyr Thr
71 50 55 60
73 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
74 65 70 75 80
76 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
77 85 90 95
79 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
80 100 105 110
82 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
83 115 120 125
85 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
86 130 135 140
88 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
89 145 150 155 160
91 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
92 165 170 175
94 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
95 180 185 190
97 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
98 195 200 205
100 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
101 210 215 220
103 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
104 225 230 235 240
106 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
107 245 250 255
109 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
110 260 265 270
112 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
113 275 280 285
115 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
116 290 295 300
118 Glu
119 305

121 (2) INFORMATION FOR SEQ ID NO: 2:

123 (i) SEQUENCE CHARACTERISTICS:

124 (A) LENGTH: 921 base pairs
125 (B) TYPE: nucleic acid
126 (C) STRANDEDNESS: double
127 (D) TOPOLOGY: unknown

129 (ii) MOLECULE TYPE: DNA (genomic)

131 (iii) HYPOTHETICAL: NO

133 (vi) ORIGINAL SOURCE:

134 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

140 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTAGA AGAAGAAGTA

60

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142	ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACTGCAGA ATTCAAAGGA	120
144	ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTGAA GAAAGACAAT	180
146	GGAGAATATA CTGTAGATGT TGCAAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA	240
148	AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT	300
150	GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA	360
152	GCATACAGAT ATGCAGATGC ATTAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA	420
154	GATAAAGGT ATACTTAAA TATTAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA	480
156	AAAGAAGAAG TTACTATTAA AGCAAACCTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA	540
158	GAATTCAAAG GAACATTGGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA	600
160	GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT	660
162	AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAGCA	720
164	AACTTAATCT ATGCAGATGG AAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA	780
166	GCAACAGCAG AAGCATAACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA	840
168	GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC	900
170	AAAAAACCAG AAGAATAATA A	921

172 (2) INFORMATION FOR SEQ ID NO: 3:

174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 434 amino acids
176 (B) TYPE: amino acid
177 (C) STRANDEDNESS: unknown
178 (D) TOPOLOGY: unknown
180 (ii) MOLECULE TYPE: protein
182 (iii) HYPOTHETICAL: NO
184 (vi) ORIGINAL SOURCE:
185 (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

189	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
191	Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
192	1 5 10 15
194	Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
195	20 25 30
197	Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
198	35 40 45
200	Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
201	50 55 60
203	Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
204	65 70 75 80
206	Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Val Thr Ile Lys Ala
207	85 90 95
209	Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
210	100 105 110
212	Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
213	115 120 125
215	Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
216	130 135 140
218	Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
219	145 150 155 160
221	Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
222	165 170 175
224	Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu

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225 180 185 190
227 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
228 195 200 205
230 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
231 210 215 220
233 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
234 225 230 235 240
236 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
237 245 250 255
239 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
240 260 265 270
242 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
243 275 280 285
245 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
246 290 295 300
248 Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
249 305 310 315 320
251 Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
252 325 330 335
254 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
255 340 345 350
257 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
258 355 360 365
260 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
261 370 375 380
263 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Lys Ala Val Asp Ala
264 385 390 395 400
266 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
267 405 410 415
269 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
270 420 425 430
272 Glu Met

275 (2) INFORMATION FOR SEQ ID NO: 4:

277 (i) SEQUENCE CHARACTERISTICS:

- 278 (A) LENGTH: 1308 base pairs
- 279 (B) TYPE: nucleic acid
- 280 (C) STRANDEDNESS: double
- 281 (D) TOPOLOGY: unknown

283 (ii) MOLECULE TYPE: DNA (genomic)

285 (iii) HYPOTHETICAL: NO

287 (vi) ORIGINAL SOURCE:

288 (A) ORGANISM: Escherichia coli L392/pHDLG, DSM 7055

292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

294 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCCAGAAA CTGATTAGA AGAAGAAGTA	60
296 ACAATCAAAG CTAACCTAAT CTTGCAAAT GGAAGCACAC AACTGCAGA ATTCAAAGGA	120
298 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT	180
300 GGAGAATATA CTGTAGATGT TGCAAGATAAA GGTTATACTT TAAATATTAA ATTGCTGGA	240
302 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT	300
304 GCAGATGGAA AAACACAAAC AGCAGAATTG AAAGGAACAT TTGAAGAAGC AACAGCAGAA	360

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306	GCATACAGAT	ATGCAGATGC	ATTAAAGAAG	GACAATGGAG	AATATACAGT	AGACGTTGCA	420
308	GATAAAGTT	ATACTTTAAA	TATTAAATT	GCTGAAAAG	AAAAAACACC	AGAAGAACCA	480
310	AAAGAAGAAG	TTACTATTAA	AGCAAACCTA	ATCTATGCAG	ATGGAAAAAC	ACAAACAGCA	540
312	GAATTCAAAG	GAACATTTGA	AGAAGCAACA	GCAGAAGCAT	ACAGATATGC	TGACTTATT	600
314	GCAAAAGAAA	ATGGTAAATA	TACAGTAGAC	GTTGCAGATA	AAGGTTATAC	TTTAAATATT	660
316	AAATTTGCTG	GAAAAGAAAA	AACACCAGAA	GAACCAAAG	AAGAAGTTAC	TATTAAGCA	720
318	AACTTAATCT	ATGCAGATGG	AAAAACTCAA	ACAGCAGAGT	TCAAAGGAAC	ATTGCAGAA	780
320	GCAACAGCAG	AAGCATACAG	ATACGCTGAC	TTATTAGCAA	AAGAAAATGG	TAAATATACA	840
322	GCAGACTTAG	AAGATGGTGG	ATACACTATT	AATATTAGAT	TTGCAGGTAA	GAAAGTTGAC	900
324	GAAAAACCGAG	AAGAACCCAT	GGACACTTAC	AAATTAATCC	TTAATGGTAA	AACATTGAAA	960
326	GGCGAAACAA	CTACTGAAGC	TGTTGATGCT	GCTACTGCAG	AAAAAGTCTT	CAAACAATAC	1020
328	GCTAACGACA	ACGGTGTGAA	CGGTGAATGG	ACTTACGACG	ATGCGACTAA	GACCTTTACA	1080
330	GTTACTGAAA	AACCAGAAGT	GATCGATGCG	TCTGAATTAA	CACCAGCCGT	GACAACATTAC	1140
332	AAACTTGTAA	TTAATGGTAA	AACATTGAAA	GGCGAAACAA	CTACTAAAGC	AGTAGACGCA	1200
334	GAAACTGCAG	AAAAAGCCTT	CAAACAATAC	GCTAACGACA	ACGGTGTGAA	TGGTGTGTTGG	1260
336	ACTTATGATG	ATGCAGACTAA	GACCTTTACG	GTAACGTAAA	TGTAATAAA		1308

338 (2) INFORMATION FOR SEQ ID NO: 5:

340 (i) SEQUENCE CHARACTERISTICS:

341	(A) LENGTH:	1332	base pairs
342	(B) TYPE:	nucleic acid	
343	(C) STRANDEDNESS:	double	
344	(D) TOPOLOGY:	unknown	

346 (ii) MOLECULE TYPE: DNA (genomic)

348 (iii) HYPOTHETICAL: NO

351 (ix) FEATURE:

352 (A) NAME/KEY: CDS

353 (B) LOCATION: 1..1329

356 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

358	AAC	GGT	GAT	GGT	AAT	CCT	AGG	GAA	GTT	ATA	GAA	GAT	CTT	GCA	GCA	AAC	48
359	Asn	Gly	Asp	Gly	Asn	Pro	Arg	Glu	Val	Ile	Glu	Asp	Leu	Ala	Ala	Asn	
360	1				5				10				15				
362	AAT	CCC	GCA	ATA	CAA	AAT	ATA	CGT	TTA	CGT	CAC	GAA	AAC	AAG	GAC	TTA	96
363	Asn	Pro	Ala	Ile	Gln	Asn	Ile	Arg	Leu	Arg	His	Glu	Asn	Lys	Asp	Leu	
364		20						25				30					
366	AAA	GCG	AGA	TTA	GAG	AAT	GCA	ATG	GAA	GTT	GCA	GGA	AGA	GAT	TTT	AAG	144
367	Lys	Ala	Arg	Leu	Glu	Asn	Ala	Met	Glu	Val	Ala	Gly	Arg	Asp	Phe	Lys	
368		35			40				45								
370	AGA	GCT	GAA	GAA	CTT	GAA	AAA	GCA	AAA	CAA	GCC	TTA	GAA	GAC	CAG	CGT	192
371	Arg	Ala	Glu	Glu	Leu	Glu	Lys	Ala	Lys	Gln	Ala	Leu	Glu	Asp	Gln	Arg	
372		50			55			60									
374	AAA	GAT	TTA	GAA	ACT	AAA	TTA	AAA	GAA	CTA	CAA	CAA	GAC	TAT	GAC	TTA	240
375	Lys	Asp	Leu	Glu	Thr	Lys	Leu	Lys	Glu	Leu	Gln	Gln	Asp	Tyr	Asp	Leu	
376		65			70			75			80						
378	GCA	AAG	GAA	TCA	ACA	AGT	TGG	GAT	AGA	CAA	AGA	CTT	GAA	AAA	GAG	TTA	288
379	Ala	Lys	Glu	Ser	Thr	Ser	Trp	Asp	Arg	Gln	Arg	Leu	Glu	Lys	Glu	Leu	
380			85			90			95								
382	GAA	GAG	AAA	AAG	GAA	GCT	CTT	GAA	TTA	GCG	ATA	GAC	CAG	GCA	AGT	CGG	336
383	Glu	Glu	Lys	Lys	Glu	Ala	Leu	Glu	Leu	Ala	Ile	Asp	Gln	Ala	Ser	Arg	
384			100			105			110								

VERIFICATION SUMMARY

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TIME: 16:22:35

Input Set : A:\402.app

Output Set: N:\CRF3\06102002\H325278A.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]